

## SEQUENCE LISTING

<110> Chang, Gwong-Jen J

<120> Nucleic Acid Vaccines for Prevention of  
Flavivirus Infection

<130> 14114.0332U3

<150> PCT/US99/12298

<151> 1999-06-03

<150> 09/701,536

<151> 2000-11-29

<150> 60/087,908

<151> 1998-06-04

<160> 31

<170> FastSEQ for Windows Version 4.0

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<223> Description of artificial sequence; note =  
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<221> CDS

<222> (25)...(48)

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48

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<223> Description of artificial sequence; note =  
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41

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51

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Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala	
15 20 25	
gga gcc atg aag ttg tgc aat ttc cag ggg aag ctt ttg atg acc atc	1047
Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile	
30 35 40	
aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga	1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly	
45 50 55 60	
gag aac aga tgc tgg ctc cgg gca atc gac gtc ggc tac atg tgt gag	1143
Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu	
65 70 75	
gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca	1191
Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro	
80 85 90	
gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat	1239
Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr	
95 100 105	
gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtc	1287
Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val	
110 115 120	
tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct	1335
Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala	
125 130 135 140	
tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac	1383
Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn	
145 150 155	
tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gca ctt ggc	1431
Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly	
160 165 170	
tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc	1479
Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu	
175 180 185	
ctg ctg ttg gtc gct ccc gct tac agt ttt aat tgt ctg gga atg ggc	1527
Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly	
190 195 200	

aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg	1575
Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu	
205 210 215 220	
gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gag aaa cca	1623
Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro	
225 230 235	
aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag	1671
Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu	
240 245 250	
gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtc	1719
Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val	
255 260 265	
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Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp	
270 275 280	
agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac	1815
Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn	
285 290 295 300	
gga tgt gga ctt ggg aag gga agc att gac aca tgt gca aaa ttc	1863
Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe	
305 310 315	
tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc	1911
Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile	
320 325 330	
aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac	1959
Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn	
335 340 345	
cat ggg aat tat tca ggc caa gtt ggg ggc tcc cag ggc gca aag ttt	2007
His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe	
350 355 360	
aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac	2055
Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr	
365 370 375 380	
gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa	2103
Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu	
385 390 395	
gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg	2151
Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg	
400 405 410	
gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca	2199

Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr			
415	420	425	
gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag ggc cac gcc			2247
Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala			
430	435	440	
aca aaa cag tcc gtt gtc ctt ggg tca cag gaa gga ggc ctc cat			2295
Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His			
445	450	455	460
cag gcg ttg gca gga gcc atc gtg gtg gag tac tca agc tca gtg aag			2343
Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Val Lys			
465	470	475	
tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct			2391
Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala			
480	485	490	
ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcc ttc gcg			2439
Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala			
495	500	505	
aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc			2487
Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser			
510	515	520	
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Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala			
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agc ctc aat gac atg acc ccc gtt ggg cgg ctg gtg aca gtg aac ccc			2583
Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro			
545	550	555	
ttc gtc gcg act tcc aag gtc agc tca aag gtg ctg gtc gag atg gaa			2631
Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu			
560	565	570	
ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag			2679
Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln			
575	580	585	
atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt			2727
Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe			
590	595	600	
tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc gac aca			2775
Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr			
605	610	615	620
gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa			2823
Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys			
625	630	635	

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gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga      2871
Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
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atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg 2919
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ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca 2967
Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
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685           690           695

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<220>  
 <223> Description of artificial sequence; note =  
 synthetic construct

<223> pCDJE 2-7

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 Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp  
 35 40 45  
 Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys  
 50 55 60  
 Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr  
 65 70 75 80  
 Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp  
 85 90 95  
 Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr  
 100 105 110  
 Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr  
 115 120 125  
 His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser  
 130 135 140  
 Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg  
 145 150 155 160  
 Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly  
 165 170 175  
 Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val  
 180 185 190  
 Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe  
 195 200 205  
 Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly  
 210 215 220  
 Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val  
 225 230 235 240  
 Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr  
 245 250 255  
 Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro  
 260 265 270  
 Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val  
 275 280 285  
 Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu  
 290 295 300  
 Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser  
 305 310 315 320  
 Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val  
 325 330 335  
 Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn His Gly Asn Tyr  
 340 345 350  
 Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro  
 355 360 365  
 Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr  
 370 375 380  
 Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val  
 385 390 395 400  
 Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His  
 405 410 415

Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn  
 420 425 430  
 Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser  
 435 440 445  
 Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala  
 450 455 460  
 Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly  
 465 470 475 480  
 His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr  
 485 490 495  
 Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala  
 500 505 510  
 Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser  
 515 520 525  
 Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp  
 530 535 540  
 Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr  
 545 550 555 560  
 Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly  
 565 570 575  
 Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His  
 580 585 590  
 Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu  
 595 600 605  
 Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe  
 610 615 620  
 Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln  
 625 630 635 640  
 Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile  
 645 650 655  
 Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala  
 660 665 670  
 Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu  
 675 680 685  
 Val Phe Leu Ala Thr Asn Val His Ala  
 690 695

&lt;210&gt; 12

&lt;211&gt; 46

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of artificial sequence; note =  
synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; 1-46

&lt;223&gt; WN 466

&lt;400&gt; 12

cttggtaccc gtctcgccgc cgtgaccctc tcgaacttcc agggca

<210> 13  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<221> misc\_feature  
<222> 1-43  
<223> CWN2444

<400> 13  
agaggcatt gcacgtgcgg acttccgcgg gcgaaaaaga aaa 43

<210> 14  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<223> JB Signal

<400> 14  
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala  
1 5 10 15  
Val Val Ile Ala Cys Ala Gly Ala  
20

<210> 15  
<211> 5308  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<221> CDS  
<222> (911)...(2987)

<221> misc\_feature  
<222> (1)...(5308)  
<223> pCBWN

<400> 15  
gacggatcgg gagatctccc gatcccctat ggtgcactct cagttacaatc tgctctgtatg 60  
ccggatagtt aagccagttat ctgtccctgt ctgtgtgtt ggaggtcgt gtagtgcg 120  
cgagaaaaat ttaagtcata acaaggcaag gtttgcaccga caattgcgtg aagaatctgc 180

ttagggttag	gcttttgcg	ctgttgcg	atgtacgggc	catatatacg	cggtgacatt	240
gattattgac	tagttatcaa	tagtaatcaa	ttacgggtc	attatgtcat	agccccata	300
tggatccg	cgttacataa	cttacggtaa	atggccccc	tggtctaccc	ccaaacgacc	360
ccgcocatt	gaacgtcaata	atgacgtatg	ttcccatagt	aaacgcataa	gggactttcc	420
atggacgtca	atgggtggag	tatttacggt	aaactgccc	cttggcagta	catcaagtgt	480
atcatatgcc	aagtacgccc	cctattgacg	ctaatgacgg	taaatggccc	gcctggdatt	540
atgcccagta	catgaccta	tgggacttcc	ctacttggca	gtacatctac	gtttagtca	600
tcgtcttac	catgttgatg	cggtttttgg	cgtatcatca	atggggctgg	atagcgtttt	660
gactcaeggg	gattpcaag	tctccacccc	attgacgtca	atggagtttgc	tttttgcac	720
caaaaatcaac	gggactttcc	aaaatgtcg	aacaactccg	ccccattgac	gcaatgggc	780
ggtaggcgtg	tacgggtgggg	ggcttatata	agcagactc	tcggcttaac	tagagaaccc	840
actgttact	ggcttattcga	attaataacg	actcaatata	ggggagaccca	agcttggta	900
cgccgcggcc	atg ggc aag	agg tcc gcc	ggc tca atc	atg tgg ctc	gca	949
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala						
1	5	10				
agc ttg gca gtt gtc ata gct tgg gca ggc gtc acc ctc tcg aac						997
Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn						
15	20	25				
ttc cag ggc aag gtg atg atg acg gta aat gct act gac gtc aca gat						1045
Phe Gln Gly Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp						
30	35	40				45
gtc atc acg att cca aca gct gct gga aag aac cta tgc att gtc aga						1093
Val Ile Thr Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg						
50	55	60				
gca atg gat gtg gga tac atg tgc gat gat act atc act tat gaa tgc						1141
Ala Met Asp Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys						
65	70	75				
cca gtg ctg tgc gtc ggt aat gat cca gaa gac atc gac tgc tgg tgc						1189
Pro Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys						
80	85	90				
aca aag tca gca gtc tac gtc agg tat gga aga tgc acc aag aca cgc						1237
Thr Lys Ser Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg						
95	100	105				
cac tca aga cgc agt cgg agg tca ctg aca gtc cag aca cac gga gaa						1285
His Ser Arg Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu						
110	115	120				125
agc act cta cgg aac aag ggg gct tgg atg gac agc acc aag gcc						1333
Ser Thr Leu Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala						
130	135	140				
aca agg tat ttg gta aaa aca gaa tca tgg atc ttg agg aac cct gga						1381
Thr Arg Tyr Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly						
145	150	155				

tat gcc ctg gtg gca gcc gtc att ggt tgg atg ctt ggg agc aac acc 1429  
 Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr  
 160 165 170  
  
 atg cag aga gtt gtg ttt gtc gtg cta ttg ctt ttg gtg gcc cca gct 1477  
 Met Gln Arg Val Val Phe Val Val Leu Leu Leu Val Ala Pro Ala  
 175 180 185  
  
 tac agc ttc aac tgc ctt gga atg agc aac aga gac ttc ttg gaa gga 1525  
 Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly  
 190 195 200 205  
  
 gtg tct gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc 1573  
 Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys  
 210 215 220  
  
 gtg act atc atg tct aag gac aag cct acc atc gat gtg aag atg atg 1621  
 Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met  
 225 230 235  
  
 aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg 1669  
 Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu  
 240 245 250  
  
 gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga 1717  
 Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly  
 255 260 265  
  
 gaa gct cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa 1765  
 Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln  
 270 275 280 285  
  
 gga gtg gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa 1813  
 Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys  
 290 295 300  
  
 gga agc att gac aca tgc gcc aaa ttt gcc tgc tct acc aag gca ata 1861  
 Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile  
 305 310 315  
  
 gga aga acc atc ttg aaa gag aat atc aag tac gaa gtg gcc att ttt 1909  
 Gly Arg Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe  
 320 325 330  
  
 gtc cat gga cca act act gtg gag tgc cac gga aac tac tcc aca cag 1957  
 Val His Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln  
 335 340 345  
  
 gtt gga gcc act cag gca ggg aga ttc agc atc act cct gcg gcg cct 2005  
 Val Gly Ala Thr Cln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro  
 350 355 360 365  
  
 tca tac aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt 2053

Ser Tyr Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys		
370	375	380
gaa cca cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt		2101
Glu Pro Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val		
385	390	395
gga aca aag acg ttc ttg gtc cat cgt gag tgg ttc atg gac ctc aac		2149
Gly Thr Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn		
400	405	410
ctc cct tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg		2197
Leu Pro Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr		
415	420	425
tta atg gag ttt gag gaa cca cac gcc acg aag cag tct gtg ata gca		2245
Leu Met Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala		
430	435	440
ttg ggc tca caa gag gga gct ctg cat caa gct ttg gtc gga gcc att		2293
Leu Gly Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile		
450	455	460
cct gtg gaa ttt tca agc aac act gtc aag ttg acg tcg ggt cat ttg		2341
Pro Val Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu		
465	470	475
aag tgt aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat		2389
Lys Cys Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr		
480	485	490
ggc gtc tgt tca aag gct ttc aag ttt ctt ggg act ccc ggc gac aca		2437
Gly Val Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr		
495	500	505
ggt cac ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga		2485
Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly		
510	515	520
cct tgc aaa gtt cct atc tcg tca gtg gct tca ttg aac gac cta acg		2533
Pro Cys Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr		
530	535	540
cca gtg ggc aga ttg gtc act gtc aac cct ttt gtt tca gtg gcc acg		2581
Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr		
545	550	555
gcc aac gct aag gtc ctg att gaa ttg gaa cca ccc ttt gga gac tca		2629
Ala Asn Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser		
560	565	570
tac ata gtg gtg ggc aga gga gaa caa cag atc aat cac cat ttg cac		2677
Tyr Ile Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His		
575	580	585

aag tct gga agc agc att ggc aaa gcc ttt aca acc acc ctc aaa gga Lys Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly 590 595 600 605	2725
gcg cag aga cta gcc gct cta gga gac aca gct tgg gac ttt gga tca Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser 610 615 620	2773
gtt gga ggg gtg ttc acc tca gtt ggg aag gct gtc cat caa gtg ttc Val Gly Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe 625 630 635	2821
gga gga gca ttc cgc tca ctg ttc gga ggc atg tcc tgg ata acg caa Gly Gly Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln 640 645 650	2869
gga ttg ctg ggg gct ctc ctg ttg tgg atg ggc atc aat gct cgt gat Gly Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Ile ASN Ala Arg Asp 655 660 665	2917
agg tcc ata gct ctc acg ttt ctc gca gtt gga gga gtt ctg ctc ttc Arg Ser Ile Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe 670 675 680 685	2965
ctc tcc gtg aac gtg cac gcc t gaaggcgcc gtcgagcat gcatactagag Leu Ser Val Asn Val His Ala 690	3017
ggccctattc tatagtgtca cttaaatgct agagctcgct gatcagccct gactgtgcct tctatgtgcg agccatctgt tgtttgccccc tccccggcgc cttcccttgac cttggaaagg gcacccatcca ctgtcccttc cttaataaaaat gaggaaatgg catcgccat tttggatagg tgtcattctt ttctgggggg tgggggtggg cggacagca aggggggggg ttggaaagac aatacgccgg atctgggggg tccggggcc tctatggctt ctggggccgg aagaaccagg tgcattaaatg aatccggcaa cgcgggggg gaggcggtt gctgtatggg gcctttccgg cttccctcgct cactgactcg ctgcgtctgg tttttggggt gccggccggat gtatcgctc actccaaaggc ggtataacgg ttatccacgg aatccggggg taacggggg aagaatcatgt gagaaaaaggc ccgaaaaaggc cggaggaaacc tggaaaaaggc cgcgttgcg ggggtttcc ataggctccg cccccctgac gacgcataca aaaaatcgccg cttaaagtccg aagggtggaa acccggacgg actataaaaaga taccggcgtt ttccccctgg aagctcccttc gtggcgcttc ctgttccggac ctggccggtt acggatacc tggccgtt tttccctgg gaaaggctgg cgcttcttcgatctcgc tgtaggtatc tgatggcggtt gttaggtcggtt cgctccaaagg tggggctgtgt gacgaaaccc cccgttcagc cggacccgtg cggccatattcc ggtaaactatc gtcttgcgtc caacccggta agacacgact tatacgccat cggcagccgc acgtggtaaca ggatggatcgac acggcggtat tgatggcggtc cttagacggat cttagatgg tggccctact acggccatcac tagaagaaca gtatgggtt tttggcgctt gctgaaggcca gtacccctcg aaaaaaaggat tggtatcgct tgatccggca aacaaaccac cggctgttagc ggtgggtttt ttttttggca gacgacgatt acggccagaaa aaaaaggatc tcaagaagat ctttgcatt tttctacggg gtcgtacgatc cgttgaaacg aaaaactccacg ttaagggtt ttggatcgta gattatcaaa aaggatcttc acctatggatc tttttaaaat aaaaatggat tttaaatca ttcaatggat attagatggaa atctggctcg acatggatcca atgttcaata acgtggggcc ctatctcggc gatctgtctt tttccgttcat ctatggatc ctgactcccc gtcgtgtaga taacatcgat acggggggcc ttacccatcg gccccggatc tgcatacgatcc cgcggagacc taacgctcacc ggtcccgat tttatcgaca taaaccaggc acggccggaaagg gccggaggcc 4517	3077

gaagtggtcc	tgcaactta	tccgcctca	tccagtctat	taattgttc	cgggaagcta	4577
gagtaagtag	ttcgcagtt	aatagttgc	gcaacgtgt	tgccattgtc	acaggcatcg	4637
tgggtcacg	ctcgctgtt	ggtatggctt	cattcagctc	cggttccaa	cgatcaaggc	4697
gaggttacatg	atccccatg	ttgtcaaaa	aacgcgttag	ctccctcggt	cctccgatcg	4757
ttgtcagaag	taagtggcc	gcagtgttat	cactcatgtt	tatggcagca	ctgcataaatt	4817
ctcttactgt	catgcccc	gtaaatgtct	tttctgtac	tgttgtagtc	tcaaccaagt	4877
cattctgaga	atagtgtatg	cggcgaccga	gttgccttg	ccggcgctca	atacgggata	4937
ataccggcc	acataggcaga	actttaaaag	tgctcatcat	tggaaaacgt	tcttcggggc	4997
gaaaacttc	aaggatctt	ccgcgtgtc	gtccaggttc	gtatgtaccc	actctgtcac	5057
ccaaactgtac	ttcagcatct	tttacttca	ccagcgtttc	tgggtgagca	aaaacaggaa	5117
ggccaaaatgc	cgccaaaaag	ggataaaggg	gcacacggaa	atgttgaaata	ctcataactt	5177
tccttttca	attattatttg	agcattttatc	agggttattt	tctcatgagc	ggatacatat	5237
ttgaatgtat	tttagaaaaat	aaacaaatag	gggttccgcg	cacattccc	cgaaaatgtc	5297
cacctgacgt	c					5308

<210> 16  
<211> 692  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<223> pCBWN

<400> 16  
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala  
1 5 10 15  
Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly  
20 25 30  
Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr  
35 40 45  
Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp  
50 55 60  
Val Gly Tyr Met Cys Asp Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu  
65 70 75 80  
Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser  
85 90 95  
Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg  
100 105 110  
Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu  
115 120 125  
Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr  
130 135 140  
Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu  
145 150 155 160  
Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg  
165 170 175  
Val Val Phe Val Val Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe  
180 185 190  
Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly  
195 200 205

Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile  
 210 215 220  
 Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu  
 225 230 235 240  
 Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val  
 245 250 255  
 Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His  
 260 265 270  
 Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val  
 275 280 285  
 Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile  
 290 295 300  
 Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr  
 305 310 315 320  
 Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly  
 325 330 335  
 Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala  
 340 345 350  
 Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr  
 355 360 365  
 Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg  
 370 375 380  
 Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys  
 385 390 395 400  
 Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp  
 405 410 415  
 Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu  
 420 425 430  
 Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser  
 435 440 445  
 Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu  
 450 455 460  
 Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg  
 465 470 475 480  
 Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys  
 485 490 495  
 Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly  
 500 505 510  
 Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys  
 515 520 525  
 Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly  
 530 535 540  
 Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala  
 545 550 555 560  
 Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val  
 565 570 575  
 Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly  
 580 585 590  
 Ser Ser Ile Gly Lys Ala Phe Thr Thr Leu Lys Gly Ala Gln Arg  
 595 600 605  
 Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly  
 610 615 620  
 Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala  
 625 630 635 640

Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu  
 645 650 655  
 Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile  
 660 665 670  
 Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val  
 675 680 685  
 Asn Val His Ala  
 690

<210> 17  
 <211> 5334  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of artificial sequence; note =  
 synthetic construct

<221> CDS  
 <222> (916)...(3007)  
  
 <221> misc\_feature  
 <222> (1)...(5334)  
 <223> pCBJE 1-14

<400> 17  
 gacggatccg gagatctccc gatccctat ggtgcactct cagataatc tgctctgatg 60  
 ccgcatagtt aagccatgt ctgcctctg cttgtgtt ggaggctcggt gagaatgtcg 120  
 cgacggaaat ttaagctaca acaaggcaag gttgtacggca caattgcatt aagaatctgc 180  
 tttaggttag gctgtttcgct ctgtttcccg atgtacgggc cagatatacg cttgtacatt 240  
 gattatttgcg tagtttattaa tagtaatcaa ttacggggcc attagttcat agcccatata 300  
 tggagttcccg ctttgcataat cttagcgtaa atggcccgcc tggctgacccg cccaaacgacc 360  
 cccgccttccat gacgtcaata atgcgtatg tttccatagt aacgcataa gggactttcc 420  
 attgacgtca atgggtggag tatttacggta aactgtccca ctggcagta catcaatgtgt 480  
 atcatatggcc aagtacggcc ctatgtacggc tcaatgtacgg taaatggccc gcttggcatt 540  
 atggccagta catgcctta tggacttttc acatgttgc acatctac gttatgtca 600  
 tggcttacatc catggtgatg cggttttggc agtacatcaa tggcgctgaa tagcggtttg 660  
 actacggggg atttccaaatg ctccacccca ttgacgtcaat tggggatgttgg ttttggcacc 720  
 aaaaatcaacg ggactttcca aatgtcgta aacactccgc cccatggacg caaatggccg 780  
 gttaggcgtgt acgggtggag gtctatataa gcaatgtctt ctggctaaatc agagaaccca 840  
 ctgtttactgt gtctatcgaa attaatacgta cttcaatcgatggagacccaa gtttggtacc 900  
 tctagacccg ccggcc atg ggc aga aag caa aac aaa aga gga aat gaa 951  
 Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu  
 1 5 10

ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg 999  
 Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala  
 15 20 25

gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc 1047  
 Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Met Thr Ile  
 30 35 40

aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga	1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Pro Thr Ser Lys Gly	
45 50 55 60	
gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag	1143
Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu	
65 70 75	
gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca	1191
Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro	
80 85 90	
gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat	1239
Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr	
95 100 105	
gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg	1287
Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val	
110 115 120	
tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct	1335
Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala	
125 130 135 140	
tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac	1383
Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn	
145 150 155	
tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc	1431
Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly	
160 165 170	
tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc	1479
Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu	
175 180 185	
ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc	1527
Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly	
190 195 200	
aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg	1575
Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu	
205 210 215 220	
gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca	1623
Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro	
225 230 235	
aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag	1671
Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu	
240 245 250	
gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg	1719

Val	Arg	Ser	Tyr	Cys	Tyr	His	Ala	Ser	Val	Thr	Asp	Ile	Ser	Thr	Val
255									260			265			

gct	cgg	tgc	ccc	acg	act	gga	gaa	gcc	cac	aac	gag	aag	cga	gct	gat	1767
Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	Ala	His	Asn	Glu	Lys	Arg	Ala	Asp	
270						275					280					

agt	agc	tat	gtg	tgc	aaa	caa	ggc	ttc	act	gac	cgt	ggg	tgg	ggc	aac	1815
Ser	Ser	Tyr	Val	Cys	Lys	Gln	Gly	Phe	Thr	Asp	Arg	Gly	Trp	Gly	Asn	
285					290				295			300				

gga	tgt	gga	ctt	ttc	ggg	aag	gga	agc	att	gac	aca	tgt	gca	aaa	ttc	1863
Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Asp	Thr	Cys	Ala	Lys	Phe	
					305				310			315				

tcc	tgc	acc	agt	aaa	gcg	att	ggg	aga	aca	atc	cag	cca	gaa	aac	atc	1911
Ser	Cys	Thr	Ser	Lys	Ala	Ile	Gly	Arg	Thr	Ile	Gln	Pro	Glu	Asn	Ile	
					320			325			330					

aaa	tac	gaa	gtt	ggc	att	ttt	gtg	cat	gga	acc	acc	act	tgc	gaa	aac	1959
Lys	Tyr	Glu	Val	Gly	Ile	Phe	Val	His	Gly	Thr	Thr	Ser	Glu	Asn		
					335			340			345					

cat	ggg	aat	tat	tca	gcg	caa	gtt	ggg	gcg	tcc	cag	gcg	gca	aag	ttt	2007
His	Gly	Asn	Tyr	Ser	Ala	Gln	Val	Gly	Ala	Ser	Gln	Ala	Ala	Lys	Phe	
					350			355			360					

aca	gta	aca	ccc	aat	gct	cct	tcg	ata	acc	ctc	aaa	ctt	ggt	gac	tac	2055
Thr	Val	Thr	Pro	Asn	Ala	Pro	Ser	Ile	Thr	Leu	Lys	Leu	Gly	Asp	Tyr	
					365			370			375			380		

gga	gaa	gtc	aca	ctg	gac	tgt	gag	cca	agg	agt	gga	ctg	aac	act	gaa	2103
Gly	Glu	Val	Thr	Leu	Asp	Cys	Glu	Pro	Arg	Ser	Gly	Leu	Asn	Thr	Glu	
					385			390			395					

gcg	ttt	tac	gtc	atg	acc	gtg	ggg	tca	aag	tca	ttt	ctg	gtc	cat	agg	2151
Ala	Phe	Tyr	Val	Met	Thr	Val	Gly	Ser	Lys	Ser	Phe	Leu	Val	His	Arg	
					400			405			410					

gag	tgg	ttt	cat	gac	ctc	gct	ccc	tgg	acg	tcc	cct	tcg	agc	aca	2199	
Glu	Trp	Phe	His	Asp	Leu	Ala	Leu	Pro	Trp	Thr	Ser	Pro	Ser	Ser	Thr	
					415			420			425					

gcg	tgg	aga	aac	aga	gaa	ctc	ctc	atg	gaa	ttt	gaa	gag	gag	cac	gcc	2247
Ala	Trp	Arg	Asn	Arg	Glu	Leu	Leu	Met	Glu	Phe	Glu	Glu	Ala	His	Ala	
					430			435			440					

aca	aaa	cag	tcc	gtt	gtt	gtc	ctt	ggg	tca	cag	gaa	gga	ggc	ctc	cat	2295
Thr	Lys	Gln	Ser	Val	Val	Ala	Leu	Gly	Ser	Gln	Glu	Gly	Gly	Leu	His	
					445			450			455			460		

cag	gcg	ttt	gca	gga	gcc	atc	gtg	gtg	gag	tac	tca	agc	tca	gtg	aag	2343
Gln	Ala	Leu	Ala	Gly	Ala	Ile	Val	Val	Glu	Tyr	Ser	Ser	Ser	Val	Lys	
					465			470			475					

tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala 480 485 490	2391
ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala 495 500 505	2439
aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser 510 515 520	2487
tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala 525 530 535 540	2535
agc ctc aat gac atg acc ccc gtt ggg cgg ctg gtg aca gtg aac ccc Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro 545 550 555	2583
ttc gtc gcg act tcc agt gcc agc tca aag gtg ctg gtc gag atg gaa Phe Val Ala Thr Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu 560 565 570	2631
ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln 575 580 585	2679
atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe 590 595 600	2727
tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc gac aca Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr 605 610 615 620	2775
gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys 625 630 635	2823
gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly 640 645 650	2871
atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met 655 660 665	2919
ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr 670 675 680	2967
ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct t aattagttg	3017

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala  
 685 690 695

agcggccgt	cgagcatgc	tctagaggc	cctattctat	agtgtcacct	aaatgtctaga	3077
gctcgctgat	cagcctcgac	tgtgccttct	agtgtccagc	catctgttgt	ttgcccctcc	3137
cccgctt	ccctggaccct	ggaagggtgc	actcccaactg	tccttctcta	ataaaaatgag	3197
gaaattgtat	cgcattgtct	gagtaggtgt	cattcttattc	tggggggtgg	ggtggggcag	3257
gacagcaagg	gggaggattg	ggaagacaat	agcaggatgc	ctggggatgc	gttggggctct	3317
atggcttcgt	aggcggaaag	aaccaggctgc	attatgtat	cgcccaacgc	gcggggagag	3377
gcggtttcg	tattgggcgc	tcttcgcgtt	cctcgcteac	tgactcgctg	cgctcggtcg	3437
ttcgcgtcg	gcgacggcta	tcactcaact	caaaagggtgt	aatacgttta	tccacagaaat	3497
caggggataa	cgccggaaag	aacatgttgag	caaaaaggcca	cgaaaaggcc	aggaacccgt	3557
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atcgacgtc	aaggcagg	ttggcggaaa	cgacggactt	ataaaagatac	cgccggatcc	3677
cccttggaa	cccttcgtgt	cgcttcgtgt	ttccgaccct	cgccgttacc	ggataccgt	3737
ccgccttct	cccttcggga	agegtggcgc	tttctcatag	ctcacgtgt	aggatatctca	3797
gttgcgtgt	ggcgttgcgc	tccaaagctgg	gtgtgtgc	cgaaacccccc	gttcacggccg	3857
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gctgttgcgt	gaagccgtt	acccctggaa	aaagaggatgg	tagcttgc	tcggcggaaac	4097
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ttaaaataaa	ataaagttttt	aatacaatct	aaatgtatata	tgatgaaact	tggtctgaca	4337
gttacaatcgt	cttaatcgt	gaggcaccata	tcttcagcgtat	ctgtcttattt	cgtttcatcca	4397
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ccagtgtcgc	aatgatatacg	cgagacccac	gtccacggc	tccagattta	tcagaataaa	4517
accagccagc	cgaaaggccc	gagcgcagaa	gtggctctgc	aactttatcc	gcctccatcc	4577
agtcttattaa	ttgttgcggc	gaagcttagag	taatgtatcc	gcccgttaat	agtttgcgc	4637
acgttgcgt	cattgttaca	ggcatctgg	tgttcacgtc	gtcggttgg	atgtttcat	4697
tcagctccgg	ttcccaacga	tcaaggcgag	ttacatgtatc	ccccatgttg	tgccaaaaaaag	4757
cggttagtc	cttcgggtct	ccgtatgttg	tcagaagtaa	gttggccgca	gtgttatac	4817
tcatgttgc	ggcagactgt	caataatttc	ttatgttcat	gcacatcgta	atgtttttt	4877
ctgtgactgg	tgtagactca	accaagatcat	tctgagaata	gtgtatgcgg	cgaccgagg	4937
gtcttgcgc	ggcgctcaata	cgggataata	ccgcggccaca	tagcagaact	ttaaaaatgtc	4997
tcatcatgg	aaaacgttct	tcggggcgaa	aactctcaag	gatcttaccc	ctgttgagat	5057
ccagtgtcgt	gtaaaccact	cgtgcaccca	actgtatctc	agcatatttt	actttcacca	5117
gcgttgcgt	gtgagcaaaa	acaggaaggc	aaaaatgcgc	aaaaaaaggga	ataagggcga	5177
cacggaaaat	ttgatatactc	atactcttc	tttttcaata	ttatgttgc	atttacagg	5237
gttattgtct	catgagcgga	tacatatttgc	aatgttatttgc	aaaaaaaataaa	caaataagggg	5297
ttccggcgcac	attttcccgaa	aaatgtccac	ctgacgt			5334

&lt;210&gt; 18

&lt;211&gt; 697

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of artificial sequence; note =  
 synthetic construct

&lt;223&gt; pCBJE 1-14

<400> 18  
Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met  
1 5 10 15  
Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys  
20 25 30  
Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp  
35 40 45  
Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys  
50 55 60  
Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr  
65 70 75 80  
Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp  
85 90 95  
Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr  
100 105 110  
Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr  
115 120 125  
His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser  
130 135 140  
Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg  
145 150 155 160  
Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly  
165 170 175  
Ser Asn Asn Gln Arg Val Val Phe Thr Ile Leu Leu Leu Val  
180 185 190  
Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe  
195 200 205  
Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly  
210 215 220  
Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val  
225 230 235 240  
Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr  
245 250 255  
Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro  
260 265 270  
Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val  
275 280 285  
Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu  
290 295 300  
Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser  
305 310 315 320  
Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val  
325 330 335  
Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn His Gly Asn Tyr  
340 345 350  
Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro  
355 360 365  
Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr  
370 375 380  
Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val  
385 390 395 400  
Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His  
405 410 415

Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn  
 420 425 430  
 Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser  
 435 440 445  
 Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala  
 450 455 460  
 Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly  
 465 470 475 480  
 His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr  
 485 490 495  
 Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala  
 500 505 510  
 Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser  
 515 520 525  
 Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp  
 530 535 540  
 Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr  
 545 550 555 560  
 Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly  
 565 570 575  
 Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His  
 580 585 590  
 Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu  
 595 600 605  
 Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe  
 610 615 620  
 Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln  
 625 630 635 640  
 Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile  
 645 650 655  
 Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala  
 660 665 670  
 Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu  
 675 680 685  
 Val Phe Leu Ala Thr Asn Val His Ala  
 690 695

<210> 19  
 <211> 5283  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of artificial sequence; note =  
 synthetic construct

<221> CDS  
 <222> (910)...(2965)

<400> 19  
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 ccgcatagtt aagccagtat ctgctccctg cttgtgttt ggaggtcgtt gagtagtgcg 60  
 cgagcaaaat ttaagtcata acaaggcaag gcttgaccga caattgcatg aagaatctgc 120  
 ttagggtagt gctgtttgcgt ctgtttcgcgt atgtacgggc cagatatacg cgttgacatt 180  
 240

gattatttgc tagttattaa tagtaatcaa ttacgggtc attagttcat agcccatata	300
tggatccg cgttacataa cttacggtaa atggccgcgc tggctgaccg cccaaacgacc	360
ccgcgcatt gacgtcaata atgacgtatg ttccatataa aacgcataa gggacttcc	420
attgacgtca atgggtggac tatttacgtt aaactgccta ctggcagta catcaagttgt	480
atcatatgcc aagtacgccc ctatggacg tcaatgacgg taaatggccc gcctggcatt	540
atgcccaga catgacccca tgggacttc ctacttgcgatcatctac gtatagtc	600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggctgga tagcggtttg	660
actcacgggg atttccaaatgcttccaa ttgacgtcaa tgggacttttggcacc	720
aaaatcaacg gggacttccaa ataatgcgtaa aacactccgc cccatggacg caaatggcg	780
gtaggcgtgt acgggtggag gtctatataa gcagagctctt ctggactaact agagaaaccca	840
ctgttactg gtctatccaa attatacga ctactatag ggagacccaa gcttggatcc	900
gcccgcgc atg ggc aag agg tcc ggc ggc tca atc atg tgg ctc gcg agc	951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	
1 5 10	
ttg gca gtt gtc ata gct ggt aca agc gct acc acc atc cac cggttgc gac	999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp	
15 20 25 30	
agg gaa gga tac atg gtt atg cgg gcc agt gga agg gac gct gca agc	1047
Arg Glu Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser	
35 40 45	
cag gtc agg gta caa aac gga acg tgc gtc atc ctg gca aca gac atg	1095
Gln Val Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met	
50 55 60	
gga gag tgg tgt gaa gat tca atc acc tac tct tgc gtc acg att gac	1143
Gly Glu Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp	
65 70 75	
cag gag gaa gaa ccc gtt gac gtg gac ttc tgc cga ggt gtt gat	1191
Gln Glu Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp	
80 85 90	
agg gtt aag tta gag tat gga cgc tgt gga agg caa gct gga tct agg	1239
Arg Val Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg	
95 100 105 110	
ggg aaa agg tct gtg gtc att cca aca cat gca caa aaa gac atg gtc	1287
Gly Lys Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val	
115 120 125	
ggg cga ggt cat gca tgg ctt aaa ggt gac aat att cga gat cat gtc	1335
Gly Arg Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val	
130 135 140	
acc cga gtc gag ggc tgg atg tgg aag aac ctt cta act gcc ggc	1383
Thr Arg Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala	
145 150 155	
att gtg gcc ttg gct tgg ctc atg gtt gat agt tgg atg gcc aga gtg	1431
Ile Val Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val	
160 165 170	

act gtc atc ctc ttg gcg ttg agt cta ggg cca gtg tac gcc acg agg	1479
Thr Val Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg	
175 180 185 190	
tgc acg cat ctt gag aac aga gat ttt gtg aca gga act caa ggg acc	1527
Cys Thr His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr	
195 200 205	
acc aga gtg tcc cta gtt ttg gaa ctt gga ggc tgc gtg acc atc aca	1575
Thr Arg Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr	
210 215 220	
gct gag ggc aag cca tcc att gat gta tgg ctc gaa gac att ttt cag	1623
Ala Glu Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln	
225 230 235	
gaa agc ccg gct gaa acc aga gaa tac tgc ctg cac gcc aaa ttg acc	1671
Glu Ser Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr	
240 245 250	
aac aca aaa gtg gag gct cgc tgt cca acc act gga ccg gcg aca ctt	1719
Asn Thr Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu	
255 260 265 270	
ccg gag gag cat cag gct aat atg gtg tgc aag aga gac caa agc gac	1767
Pro Glu Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp	
275 280 285	
cgt gga tgg gga aac cac tgc ggg ttt ttt ggg aag ggc agt ata gtg	1815
Arg Gly Trp Gly Asn His Cys Gly Phe Phe Gly Lys Ser Ile Val	
290 295 300	
gct tgt gca aag ttt gaa tgc gag gaa gca aaa aaa gct gtg ggc cac	1863
Ala Cys Ala Lys Phe Glu Cys Glu Ala Lys Lys Ala Val Gly His	
305 310 315	
gtc tat gac tcc aca aag atc acg tat gtt gtc aag gtt gag ccc cac	1911
Val Tyr Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His	
320 325 330	
aca ggg gat tac ttg gct gca aat gag acc aat tca aac agg aaa tca	1959
Thr Gly Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser	
335 340 345 350	
gca cag ttt acg gtg gca tcc gag aaa gtg atc ctg cgg ctc ggc gac	2007
Ala Gln Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp	
355 360 365	
tat gga gat gtg tgc ctg acg tgt aaa gtg gca agt ggg att gat gtc	2055
Tyr Gly Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val	
370 375 380	
gcc caa act gtg gtg atg tca ctc gac agc agc aag gac cac ctg cct	2103

Ala Gln Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro		
385	390	395
tct gca tgg caa gtg cac cgt gac tgg ttt gag gac ttg gcg ctg ccc		2151
Ser Ala Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro		
400	405	410
tgg aaa cac aag gac aac caa gat tgg aac agt gtg gag aaa ctt gtg		2199
Trp Lys His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val		
415	420	425
gaa ttt gga cca cca cat gct gtg aaa atg gat gtt ttc aat ctg ggg		2247
Glu Phe Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly		
435	440	445
gac cag acg gct gtg ctg ctc aaa tca ctg gca gga gtt ccg ctg gcc		2295
Asp Gln Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala		
450	455	460
agt gtg gag ggc cag aaa tac cac ctg aaa agc ggc cat gtt act tgt		2343
Ser Val Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys		
465	470	475
gat gtg gga ctg gaa aag ctg aaa ctg aaa ggc aca acc tac tcc atg		2391
Asp Val Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met		
480	485	490
tgt gac aaa gca aag ttc aaa tgg aag aga gtt cct gtg gac agc ggc		2439
Cys Asp Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly		
495	500	505
cat gac aca gta gtc atg gag gta tca tac aca gga agc gac aag cca		2487
His Asp Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro		
515	520	525
tgt cgg atc ccg gtg cgg gct gtg gca cat ggt gtc cca gcg gtt aat		2535
Cys Arg Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn		
530	535	540
gta gcc atg ctc ata acc ccc aat cca acc att gaa aca aat ggt ggc		2583
Val Ala Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly		
545	550	555
gga ttc ata gaa atg cag ctg cca cca ggg gat aac atc atc tat gtg		2631
Gly Phe Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val		
560	565	570
gga gac ctt agc cag cag tgg ttt cag aaa ggc agt acc att ggt aga		2679
Gly Asp Leu Ser Gln Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Arg		
575	580	585
atg ttt gaa aaa acc cgc agg gga ttg gaa agg ctc tct gtg gtt gga		2727
Met Phe Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly		
595	600	605



tcatcattgg	aaaacgttct	tcggggcgaa	aacttccaag	gatcttacgg	ctgttgagat	5005
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cacggaaaatg	ttgaatactc	atactttcc	tttttcaata	tttatttttt	tttttttttt	5185
gtttatgttgc	catggcgccg	tatcatatgg	aatgttattt	tttttttttt	tttttttttt	5245
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<210> 20  
<211> 681  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

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Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys Asn Arg
20 25 30
Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser
35 40 45
Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys Tyr Trp
50 55 60
Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu
65 70 75 80
Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg
85 90 95
Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg
100 105 110
Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg
115 120 125
Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Glu Leu Gln Lys
130 135 140
Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu
145 150 155 160
Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile
165 170 175
Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile
180 185 190
Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp
195 200 205
Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro
210 215 220
Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg
225 230 235 240
Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val
245 250 255
Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu
260 265 270
Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly
275 280 285

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Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys  
 290 295 300  
 Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln  
 305 310 315 320  
 Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys  
 325 330 335  
 Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu  
 340 345 350  
 Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu  
 355 360 365  
 Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala  
 370 375 380  
 Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp  
 385 390 395 400  
 Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met  
 405 410 415  
 His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val  
 420 425 430  
 Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly  
 435 440 445  
 Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu  
 450 455 460  
 His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu  
 465 470 475 480  
 Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys  
 485 490 495  
 Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val  
 500 505 510  
 Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu  
 515 520 525  
 Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala  
 530 535 540  
 Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly  
 545 550 555 560  
 Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln  
 565 570 575  
 Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met  
 580 585 590  
 Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe  
 595 600 605  
 Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr  
 610 615 620  
 Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile  
 625 630 635 640  
 Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr  
 645 650 655  
 Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met  
 660 665 670  
 Met Phe Leu Ser Leu Gly Val Gly Ala  
 675 680

<210> 21  
 <211> 5304  
 <212> DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of artificial sequence; note =  
synthetic construct

&lt;221&gt; CDS

&lt;222&gt; (910)...(2986)

&lt;400&gt; 21

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cccgatagtt	aaggcaggat	ctgtccctg	cttgggtgtt	ggaggctgct	gagtagtgcg	120							
cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcgtg	aagaatctgc	180							
tttaggttag	gctgtttcg	ctgttgcgc	atgtacggcc	catgatatacg	cgttgacatt	240							
gattattgtac	tagtttataa	tagtaatcaa	ttacgggttc	attatgtcat	agccccatata	300							
tggagttcg	cgttacataa	cttacggtaa	atggccggcc	ttggctgaccg	ccaaacgacc	360							
cccgccattt	gacgcttaata	atgacgtatg	ttcccatatgt	aaaggccataa	gggactttcc	420							
atggacgtca	atgggtggac	tattttacgtt	aaactgcoca	cttggcagta	catcaagtgt	480							
atcatatgcc	aagtacgccc	cctatttgacg	tcaatgacgg	taaatggccc	gcctggcatt	540							
atggccgat	catggaccta	ttgggacttcc	ctactttggca	gtacatctac	gtatttagtcg	600							
tcgttattac	catgttgcgat	cgggttttgc	atgtatcaa	ttggcgttgg	taegcggttg	660							
actcacgggg	atttccaaatg	cttccacccca	ttgacgtcaa	ttgggattttgc	ttttggcacc	720							
aaaatcaacg	ggactttccaa	aatatcgatg	acaactccgc	ccccatggacg	caaatggccg	780							
gtaggcggt	acgggtggag	gtctatataa	gcagactctc	ttggcttaact	agagaacccca	840							
ctgttactg	gtcttacgtaa	attatacga	ctcaatatacg	cgagacccaa	gttggtacc	900							
gccccccccc	atg ggc aag	agg tcc gcc	gtc atc atg	tgg ctc gcg	agc	951							
Met	Gly	Lys	Arg	Ser	Ala	Gly	Ser	Ile	Met	Trp	Leu	Ala	Ser
1	5					10							

ttg	gca	gtt	gtc	ata	gct	ggt	aca	agc	gct	ttt	cag	tta	tca	acc	tat		999
Leu	Ala	Val	Val	Ile	Ala	Gly	Thr	Ser	Ala	Leu	Gln	Leu	Ser	Thr	Tyr		
15	20			25		30											

cag	ggg	aaa	gtt	tta	atg	tca	atc	aac	aag	act	gac	gct	caa	agc	gcc		1047
Gln	Gly	Val	Leu	Met	Ser	Ile	Asn	Lys	Thr	Asp	Ala	Gln	Ser	Ala			
35			40			45											

ata	aac	att	cct	agt	gcc	aac	ggg	gca	aac	act	tgc	att	gttgc	agg	gct		1095
Ile	Asn	Ile	Pro	Ser	Ala	Asn	Gly	Ala	Asn	Thr	Cys	Ile	Val	Arg	Ala		
50			55			60											

cta	gat	gtt	ggg	gtc	atg	tgc	aaa	gat	gac	atc	aca	tac	ctg	tgc	cca		1143
Leu	Asp	Val	Gly	Val	Met	Cys	Lys	Asp	Asp	Ile	Thr	Tyr	Leu	Cys	Pro		
65			70			75											

gtt	ctt	tca	gct	gga	aat	gat	ccc	gag	gac	att	gac	tgt	tgg	tgt	gac		1191
Val	Leu	Ser	Ala	Gly	Asn	Asp	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Asp		
80			85			90											

gtc	gaa	gag	gtt	tgg	tgc	cac	tac	ggc	aga	tgc	acg	cgc	atg	gga	cat		1239
Val	Glu	Glu	Val	Trp	Val	His	Tyr	Gly	Arg	Cys	Thr	Arg	Met	Gly	His		
95			100			105							110				

tcg	agg	cgt	agc	cga	cgg	tca	atc	tct	gtg	cag	cat	cat	gga	gat	tcc		1287
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	------

Ser Arg Arg Ser Arg Arg Ser Ile Ser Val Gln His His His Gly Asp Ser			
115	120	125	
aca ctg gca aca aag aac acg cca tgg ttg gac acc gtg aaa acc acc		1335	
Thr Leu Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr			
130	135	140	
aaa tac ttg aca aaa gta gaa aac tgg ttg cgc aat cct gga tat		1383	
Lys Tyr Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr			
145	150	155	
gcc cta gtt gcg ctg gcg att gga tgg atg ctc ggt agc aac aac aca		1431	
Ala Leu Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr			
160	165	170	
cag aga gtg gtt ttt gtg atc atg ctg atg ctg att gct ccg gca tac		1479	
Gln Arg Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr			
175	180	185	190
agc ttc aac tgt ctg gga aca tca aac agg gac ttt gtc gag gga gcc		1527	
Ser Phe Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala			
195	200	205	
agt ggg gca aca tgg att gac ttg gta ctt gaa ggg gga agc tgt gtc		1575	
Ser Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Ser Cys Val			
210	215	220	
aca gtg atg gca cca gag aaa cca aca ctg gac ttc aaa gtg atg aag		1623	
Thr Val Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys			
225	230	235	
atg gag gct acc gag tta gcc act gtg cgt gag tat tgt tac gaa gca		1671	
Met Glu Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala			
240	245	250	
acc ttg gac acg ctg tca aca gtg gca agg tgc ccc aca aca gga gaa		1719	
Thr Leu Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu			
255	260	265	270
gct cac aac acc aaa agg agt gac cca aca ttt gtc tgc aaa aga gat		1767	
Ala His Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp			
275	280	285	
gtt gtg gac cgc gga tgg ggt aac gga tgt ggt ctg ttt gga aaa ggg		1815	
Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly			
290	295	300	
agc att gac aca tgc gct aag ttc aca tgc aaa aac aag gca aca ggg		1863	
Ser Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly			
305	310	315	
aag acg atc ttg aga gaa aac atc aag tat gag gtt gca atc ttt gtg		1911	
Lys Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val			
320	325	330	

cat ggt tca acg gac tct acg tca cat ggc aat tac tct gag cag att His Gly Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile 335 340 345 350	1959
gga aaa aac caa gcg gct aga ttc acc ata agc ccg caa gca ccg tcc Gly Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser 355 360 365	2007
ttt acg gcc aac atg ggc gag tat gga aca gtt acc att gat tgt gaa Phe Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu 370 375 380	2055
gca aga tca gga atc aac acg gag gat tat tat gtt ttc act gtc aag Ala Arg Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys 385 390 395	2103
gag aag tca tgg cta gtg aac agg gac tgg ttt cac gac ttg aac ctt Glu Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu 400 405 410	2151
cca tgg acg agc cct gcc aca act gat tgg cgc aac aga gaa aca ctg Pro Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu 415 420 425 430	2199
gtg gaa ttt gag gaa ccg cat gcc acc aag caa act gta gta gcc cta Val Glu Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu 435 440 445	2247
gga tcg caa gaa ggt gcc ctg cac aca gca ttg gct gga gcc att cca Gly Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro 450 455 460	2295
gcc act gtt agc agc tca acc cta acc ttg caa tca ggg cat ttg aaa Ala Thr Val Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys 465 470 475	2343
tgc aga gct aag ctt gac aag gtc aaa atc aag gga acg aca tat ggc Cys Arg Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly 480 485 490	2391
atg tgt gac tct gcc ttc acc ttc agc aag aac cca act gac aca ggg Met Cys Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly 495 500 505 510	2439
cac ggg aca gtg att gtg gaa ctg cag tat act gga agc aac gga ccc His Gly Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro 515 520 525	2487
tgc cga gtt ccc atc tcc gtg act gca aac ctc atg gat ttg aca ccg Cys Arg Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro 530 535 540	2535
gtt gga aga ttg gtc acg gtc aat ccc ttt ata agc aca ggg gga ccg	2583

Val Gly Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala		
545	550	555
aac aac aag gtc atg atc gaa gtt gaa cca ccc ttt ggc gat tct tac		2631
Asn Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr		
560	565	570
atc gtc gtc gga aga ggc acc acc cag att aac tac cac tgg cac aaa		2679
Ile Val Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys		
575	580	585
gag gga agc agc att ggg aag gct ttg gcg acc aca tgg aaa gga gcc		2727
Glu Gly Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala		
595	600	605
caa cgg cta gcc gtc tta ggg gac aca gcg tgg gac ttt gga tct att		2775
Gln Arg Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile		
610	615	620
gga gga gtt ttc aat tca att ggc aaa gct gtc cac caa gtt ttc gga		2823
Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly		
625	630	635
gga gcg ttc agg act ctg ttc ggg gga atg tcc tgg atc aca cag ggg		2871
Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly		
640	645	650
cta ctt gga gct ctt ctc ctg tgg atg ggg ttg cag gcc cgc gac agg		2919
Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg		
655	660	665
agc atc tcg ctg act cta ctg gct gtc gga ggg att ctc atc ttt ctg		2967
Ser Ile Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu		
675	680	685
gca acc agc gtg caa gcc t gagcggccgc tcgagcatgc atctagaggg		3016
Ala Thr Ser Val Gln Ala		
690		
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aactctcaag	gatcttaccc	ctgttgcgc	ccatgtcgat	gtacccact	ctgtcaccacca	5056
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aatgtatata	aaaaataaaa	caaataagggg	ttccgcgcac	attttcccg	aaagtgcac	5296
ctgacgtc						5304

<210> 22  
 <211> 692  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of artificial sequence; note =  
 synthetic construct

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 1 5 10 15  
 Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr Gln Gly  
 20 25 30  
 Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala Ile Asn  
 35 40 45  
 Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala Leu Asp  
 50 55 60  
 Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro Val Leu  
 65 70 75 80  
 Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp Val Glu  
 85 90 95  
 Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His Ser Arg  
 100 105 110  
 Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser Thr Leu  
 115 120 125  
 Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr Lys Tyr  
 130 135 140

Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr Ala Leu  
 145 150 155 160  
 Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr Gln Arg  
 165 170 175  
 Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr Ser Phe  
 180 185 190  
 Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser Gly  
 195 200 205  
 Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr Val  
 210 215 220  
 Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met Glu  
 225 230 235 240  
 Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr Leu  
 245 250 255  
 Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala His  
 260 265 270  
 Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val Val  
 275 280 285  
 Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile  
 290 295 300  
 Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys Thr  
 305 310 315 320  
 Ile Leu Arg Glu Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly  
 325 330 335  
 Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile Gly Lys  
 340 345 350  
 Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe Thr  
 355 360 365  
 Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala Arg  
 370 375 380  
 Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys Glu Lys  
 385 390 395 400  
 Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro Trp  
 405 410 415  
 Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val Glu  
 420 425 430  
 Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly Ser  
 435 440 445  
 Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala Thr  
 450 455 460  
 Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys Arg  
 465 470 475 480  
 Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met Cys  
 485 490 495  
 Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly His Gly  
 500 505 510  
 Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys Arg  
 515 520 525  
 Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val Gly  
 530 535 540  
 Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn Asn  
 545 550 555 560  
 Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val  
 565 570 575

Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu Gly  
 580 585 590  
 Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala Gln Arg  
 595 600 605  
 Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly  
 610 615 620  
 Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala  
 625 630 635 640  
 Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu  
 645 650 655  
 Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg Ser Ile  
 660 665 670  
 Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu Ala Thr  
 675 680 685  
 Ser Val Gln Ala  
 690

&lt;210&gt; 23

&lt;211&gt; 5271

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of artificial sequence; note =  
synthetic construct

&lt;221&gt; CDS

&lt;222&gt; (910)...(2953)

&lt;400&gt; 23

gacggatcg gagatctccc gatccccat ggtcgactct cagtacaatc tgctctgtatg 60  
 ccgcataatg aaggcaggat ctgtccctgt ctgtgtgtt ggagggtcgct gagtagtgcg 120  
 cgagcaaat ttaatgtaca acaaggcaag gttgaccga caattgcatg aagaatctgc 180  
 tttaggttag gctgtttcgct ctgtttcgct atgtacggc catatatacg cttgtacattc 240  
 gattatttgcg tagttttaaa tagtaatcaa ttacggggctt attagttcat agcccatata 300  
 tggatgtccg cgttacatcaa cttaggttacatggccctc tggctgaccg cccaaacgacc 360  
 cccgcattt gacgttacatc atgacgtatg tttccatagt aacgcataa gggactttcc 420  
 attgacgtca atgggtggac tattttacggt aaactgcaca ctggcagta catcaagtgt 480  
 atcatatggc aagtacggcc cttatgtacgg tcaatgtacgg taaatggccc gcctggcatt 540  
 atgcggatgtt catgtccat tggggatcttccatcttgcgtt acatcatctac gttagatca 600  
 tcgtcttacatc catgggtatg cgggtttggc agtacatcaa tggggctgttgc tggcggttt 660  
 actcacgggg atttttttttttgcgttacatggatggatggatggatggatggatggatggatgg 720  
 aaaaatcaacgg ggactttccaa ataatgtcataa acaactccgc cccatgtacgg caaatggcg 780  
 gtaggcgtgt acgggtggag gtctatataa gcaagatctt ctggctaaact agagaaccca 840  
 ctgttttttttgcgttacgttgcgttacatggatggatggatggatggatggatggatggatggatgg 900  
 gcccggccatc atggcggccatc atggcggccatc atggcggccatc atggcggccatc atggcggccatc 951  
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser  
 1 5 10

ttg gca gtt gtc ata gct ggt aca agc gct gtg acc ttg gtg cgg aaa 999  
 Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys  
 15 20 25 30

aac aga tgg ttg ctc cta aat gtg aca tct gag gac ctc ggg aaa aca 1047

Asn Arg Trp Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr			
35	40	45	
ttc tct gtg ggc aca ggc aac tgc aca aca aac att ttg gaa gcc aag			1095
Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys			
50	55	60	
tac tgg tgc cca gac tca atg gaa tac tac aac tgt ccc aat ctc aat cca			1143
Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro			
65	70	75	
aga gag gag cca gat gac att gat tgc tgg tgc tat ggg gtg gaa aac			1191
Arg Glu Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn			
80	85	90	
gtt aga gtc gca tat ggt aag tgt gac tca gca ggc agg tct agg agg			1239
Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg			
95	100	105	110
tca aca agg gcc att gag ttg cct acg cat gaa aac cat ggt ttg aag			1287
Ser Arg Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys			
115	120	125	
acc cgg caa gaa aaa tgg atg act gga aga atg ggt gaa agg caa ctc			1335
Thr Arg Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu			
130	135	140	
caa aag att gag aga tgg ttc gtg agg aac ccc ttt ttt gca gtg acg			1383
Gln Lys Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr			
145	150	155	
gct ctg acc att gcc tac ctt gtg gga agc aac atg acg caa cga gtc			1431
Ala Leu Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val			
160	165	170	
gtg att gcc cta ctg gtc ttg gct gtt ggt ccg gcc tac tca gct cac			1479
Val Ile Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His			
175	180	185	190
tgc att gga att act gac agg gat ttc att gag ggg gtg cat gga gga			1527
Cys Ile Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly			
195	200	205	
act tgg gtt tca gct acc ctg gag caa gac aag tgt gtc act gtt atg			1575
Thr Trp Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met			
210	215	220	
gcc cct gac aag cct tca ttg gac atc tca cta gag aca gta gcc att			1623
Ala Pro Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile			
225	230	235	
gat aga cct gct gag gtg agg aaa gtg tgt tac aat gca gtt ctc act			1671
Asp Arg Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr			
240	245	250	

cat gtg aag att aat gac aag tgc ccc agc act gga gag gcc cac cta	1719
His Val Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu	
255 260 265 270	
gct gaa gag aac gaa ggg gac aat gcg tgc aag cgc act tat tct gat	1767
Ala Glu Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp	
275 280 285	
aga ggc tgg ggc aat ggc tgc aat ggc cta ttt ggg aaa ggg agc att gtg	1815
Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val	
290 295 300	
gca tgc gcc aaa ttc act tgc aat tcc atg agt ttg ttt gag gtt	1863
Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val	
305 310 315	
gat cag acc aaa att cag tat gtc atc aga gca caa ttg cat gta ggg	1911
Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly	
320 325 330	
gcc aag cag gaa aat tgg act acc gac att aag act ctc aag ttt gat	1959
Ala Lys Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp	
335 340 345 350	
gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct	2007
Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala	
355 360 365	
aca ctg gaa tgc cag gtg caa act gcg gtg gac ttt ggt aac agt tac	2055
Thr Leu Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr	
370 375 380	
atc gct gag atg gaa aca gag agc tgg ata gtg gac aga cag tgg gcc	2103
Ile Ala Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala	
385 390 395	
cag gac ttg acc ctg cca tgg cag agt gga agt ggc ggg gtg tgg aga	2151
Gln Asp Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Val Trp Arg	
400 405 410	
gag atg cat cat ctt gtc gaa ttt gaa cct ccg cat gcc gcc act atc	2199
Glu Met His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile	
415 420 425 430	
aga gta ctg gcc ctg gga aac cag gaa ggc tcc ttg aaa aca gct ctt	2247
Arg Val Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu	
435 440 445	
act ggc gca atg agg gtt aca aag gac aca aat gac aac aac ctt tac	2295
Thr Gly Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr	
450 455 460	
aaa cta cat ggt gga cat gtt tct tgc aga gtg aaa ttg tca gct ttg	2343

Lys Leu His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu		
465	470	475
aca ctc aag ggg aca tcc tac aaa ata tgc act gac aaa atg ttt ttt		2391
Thr Leu Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe		
480	485	490
gtc aag aac cca act gac act ggc cat ggc act gtt gtg atg cag gtg		2439
Val Lys Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val		
495	500	505
aaa gtg tca aaa gga gcc ccc tgc agg att cca gtg ata gta gct gat		2487
Lys Val Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp		
515	520	525
gat ctt aca gcg gca atc aat aaa ggc att ttg gtt aca gtt aac ccc		2535
Asp Leu Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro		
530	535	540
atc gcc tca acc aat gat gat gaa gtg ctg att gag gtg aac cca cct		2583
Ile Ala Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro		
545	550	555
ttt gga gac agc tac att atc gtt ggg aga gga gat tca cgt ctc act		2631
Phe Gly Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr		
560	565	570
tac cag tgg cac aaa gag gga agc tca ata gga aag ttg ttc act cag		2679
Tyr Gln Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln		
575	580	585
acc atg aaa ggc gtg gaa cgc ctg gcc gtc atg gga gac acc gcc tgg		2727
Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp		
595	600	605
gat ttc agc tcc gct gga ggg ttc ttc act tcg gtt ggg aaa gga att		2775
Asp Phe Ser Ser Ala Gly Gly Phe Thr Ser Val Gly Lys Gly Ile		
610	615	620
cat acg gtg ttt ggc tct gcc ttt cag ggg cta ttt ggc ggc ttg aac		2823
His Thr Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn		
625	630	635
tgg ata aca aag gtc atc atg ggg ggc gta ctt ata tgg gtt ggc atc		2871
Trp Ile Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile		
640	645	650
aac aca aga aac atg aca atg tcc atg agc atg atc ttg gta gga gtg		2919
Asn Thr Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val		
655	660	665
atc atg atg ttt ttg tct cta gga gtt ggg ggc t gacggccgc		2963
Ile Met Met Phe Leu Ser Leu Gly Val Gly Ala		
675	680	

tcgagcatgc atctagaggg ccctattctta tagtgtcacc taaatcttag agctcgctga	3023
tcagcctcga ctgtgccttc tagttgcagc ccatctgtt tttgccttc cccctgcct	3083
tccttgaccc tggaaagggtc cactcccaact gtccttctt aataaaatgt gaaatttgc	3143
tcgcattgtc tgtaggttg tcattctatt ctgggggggtg gggggggggca ggacagcaag	3203
ggggaggatt gggaaagacaa tagcaggat gctggggatc cgggtggctc tatggcttc	3263
gaggcgaaaaa gaacagctgc attaatgtat cggccaaacgc gggggggagag ggggtttgc	3323
tattttggcgc tccttcgtt ctcgtcctac tgactcgctg cgtctcgctg ttccggctcg	3383
gcgagcgta tcagtcactaa caaaggcggt aatacggttacccagaat cagggataa	3443
cgcaggaaag aacatgtgag caaaaggcca gcaaaaggcc aggaaccgtt aaaaaggccgc	3503
gttgcgtggc ttttttccata ggctccgcggcc cccctggacg catcacaaaa atcgacgtt	3563
aagtccagg tggccaaaaacc cgcaggactt aataagatacc cggcggttcc cccctggaa	3623
ctccctctgt cgctctctgt ttccgaccct gccgttacc ggataacctgt cgccttttct	3683
ccacccggaa agctcgccggc ttccaaatgtt ctcacgttgc aggtatctca gttccgtgt	3743
ggtcgtcgcc ttcggatgttgc gtcgtgttgc gaaacccccc gttccggcc accgtcgcc	3803
cttataccgtt aactatcgcc ttgagttccaa cccggtaaga cagacttat cgcacttgc	3863
agcggccactt ggttacacggg tttagcaggag gaggatgttgc gggcggtgtca cagagtctt	3923
gaatgttggc cttactatcg cgtacatctg aaggacatgtt gttgtatctt ggcgtctgt	3983
gaaggccgtt accttcggaa aaagagttgg tagctcttgc tccggcaaaac aaaaaccacgc	4043
ttgttcgtgtt ggtttttttt ttgcacggaa gcaatgttgc cgcaggaaaaaa aaggatctca	4103
agaatgttcc ttgtatgttgc ctacggggcc ttagcgttgc tggaaaggaa attacgttta	4163
agggattttgc gtcatgagat tatcaaaaag gatcttcacc tagatcttt taaattaaaa	4223
atgtatgtttttaa aatagtatata tgatgttataat ttgtgttgcata gttaccaatg	4283
cttaatcgtt gaggccacca ttcgtcgat cttgtcttattt cttgtcatccatccatggcttgc	4343
actcccccgtc ttgttagatata ctacgatatacg gggggccatccatccatggcc ccaatgttgc	4403
aatgtatcccg cggacccccc gtcacccggc tccagatataa tccagaataaa accagccaggc	4463
cggaggccggc gaggccggaa ggggttccatccatccatggccatccatccatggccatccatgg	4523
ttgttgcggg gaaatgttgc tttgtatgttgc gccaggatataat ttgttgcgc gatgttgc	4583
cattgttgcata ggctatgttgc ttgttgcgttgc gttgttgcgttgc ttagtcccg	4643
cttcggatccatccatggccatccatggccatccatggccatccatggccatccatggccatccatgg	4703
tttcgggttccatccatggccatccatggccatccatggccatccatggccatccatggccatccatgg	4763
ggcgcactgttccatccatggccatccatggccatccatggccatccatggccatccatggccatccatgg	4823
ttgtatgttgc tttgtatgttgc ggggttccatccatggccatccatggccatccatggccatccatgg	4883
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tttgcggccatccatggccatccatggccatccatggccatccatggccatccatggccatccatggccatccatgg	5243
tttgcggccatccatggccatccatggccatccatggccatccatggccatccatggccatccatggccatccatgg	5271

&lt;210&gt; 24

&lt;211&gt; 681

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of artificial sequence; note =  
synthetic construct

&lt;400&gt; 24

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala

1

5

10

15

Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys Asn Arg  
 20 25 30  
 Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser  
 35 40 45  
 Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys Tyr Trp  
 50 55 60  
 Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu  
 65 70 75 80  
 Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg  
 85 90 95  
 Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg  
 100 105 110  
 Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg  
 115 120 125  
 Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys  
 130 135 140  
 Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu  
 145 150 155 160  
 Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile  
 165 170 175  
 Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile  
 180 185 190  
 Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp  
 195 200 205  
 Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro  
 210 215 220  
 Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg  
 225 230 235 240  
 Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val  
 245 250 255  
 Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu  
 260 265 270  
 Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly  
 275 280 285  
 Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys  
 290 295 300  
 Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln  
 305 310 315 320  
 Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys  
 325 330 335  
 Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu  
 340 345 350  
 Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu  
 355 360 365  
 Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala  
 370 375 380  
 Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp  
 385 390 395 400  
 Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Val Trp Arg Glu Met  
 405 410 415  
 His His Leu Val Glu Phe Glu Pro His Ala Ala Thr Ile Arg Val  
 420 425 430  
 Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly  
 435 440 445

Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Leu Tyr Lys Leu  
450 455 460  
His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu  
465 470 475 480  
Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys  
485 490 495  
Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val  
500 505 510  
Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu  
515 520 525  
Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala  
530 535 540  
Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly  
545 550 555 560  
Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln  
565 570 575  
Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met  
580 585 590  
Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe  
595 600 605  
Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr  
610 615 620  
Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile  
625 630 635 640  
Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr  
645 650 655  
Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met  
660 665 670  
Met Phe Leu Ser Leu Gly Val Gly Ala  
675 680

<210> 25  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<221> misc\_feature  
<222> 1-35  
<223> POW 454

<400> 25  
aaaagaaaaa gcgctaccac catccaccgg gacag

35

<210> 26  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<221> misc\_feature  
<222> 1-41  
<223> CPOW 2417

<400> 26  
actgttaccc tcaacccgt actcgccggc gaaaaagaaa a

41

<210> 27  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<223> Modified JE Signal

<400> 27  
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala  
1 5 10 15  
Val Val Ile Ala Gly Thr Ser Ala  
20

<210> 28  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<221> misc\_feature  
<222> 1-36  
<223> YF 482

<400> 28  
aaaagaaaaa ggcgtgtgac cttgggtgcgg aaaaac

36

<210> 29  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

SEARCHED  
INDEXED  
SERIALIZED  
FILED  
FEB 12 2004  
FBI - BOSTON

<221> misc\_feature  
<222> 1-41  
<223> CYF 2433

<400> 29  
acagagatcc tcaaccccgc actcgccggc gaaaaagaaa a 41

<210> 30  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<221> misc\_feature  
<222> 1-41  
<223> SLE 463

<400> 30  
aaaagaaaaa gcgcgttgca gttatcaacc tatcagggga a 41

<210> 31  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<221> misc\_feature  
<222> 1-40  
<223> CSLE 2477

<400> 31  
accgttggtc gcacgttcgg actcgccggc gaaaaagaaa 40